SEQUENCE LISTING

<110> Hart, Derek N J

<120> Enzyme having S-adenosyl-L-homocysteine hydrolase
      (AHCY) type activity

<130> 24305 MRB

<140> JP 516412/98
<141> 1999-05-19

<150> PCT/NZ97/00133
<151> 1997-10-06

<150> NZ 299507
<151> 1996-10-04

<160> 2

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<223> Open reading frame extends without a stop codon
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      initiation codon has yet to be identified.

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   Arg Gly Gln Val Gly Ala Arg Ser Cys Cys Phe Trp Phe Ser Cys
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ggc cac cgt cgc tgt ccg gct gcc ttg ggc tgc cga aca gac aag gcg   95
Gly His Arg Arg Cys Pro Ala Ala Leu Gly Cys Arg Thr Asp Lys Ala
            20   25   30

tgg gcc aca gca cct cag aag ccg acg cag ctc gac gca ggg gcc ggc   143
Trp Ala Thr Ala Pro Gln Lys Pro Thr Gln Leu Asp Ala Gly Ala Gly
        35   40   45

agg agg gtg ggc gat cgc gtg tcg gag ggc gcc gcg cgg gca ggc ggg   191
Arg Arg Val Gly Asp Arg Val Ser Glu Gly Ala Ala Arg Ala Gly Gly
        50   55   60

cgg gcg cca gag ggg gaa aga ggc ggg ggc ggc ggg tca gcc gct ggc   239
Arg Ala Pro Glu Gly Glu Arg Gly Gly Gly Gly Gly Ser Ala Ala Gly
    65   70   75

cgg gcc ggc ggg gga atg tcg atg cct gac gcg atg ccg ctg ccc ggg   287
Arg Ala Gly Gly Gly Met Ser Met Pro Asp Ala Met Pro Leu Pro Gly
    80   85   90   95

gtc ggg gag gag ctg aag cag gcc aag gag atc gag gac gcc gag aag   335
Val Gly Glu Glu Leu Lys Gln Ala Lys Glu Ile Glu Asp Ala Glu Lys

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                  100                      105                      110

tac tcc ttc atg gcc acc gtc acc aag gcg ccc aag aag caa atc cag    383
Tyr Ser Phe Met Ala Thr Val Thr Lys Ala Pro Lys Lys Gln Ile Gln
                115                      120                      125

ttt gct gat gac atg cag gag ttc acc aaa ttc ccc acc aaa act ggc    431
Phe Ala Asp Asp Met Gln Glu Phe Thr Lys Phe Pro Thr Lys Thr Gly
                130                      135                      140

cga aga tct ttg tct cgc tcg atc tca cag tcc tcc act gac agc tac    479
Arg Arg Ser Leu Ser Arg Ser Ile Ser Gln Ser Ser Thr Asp Ser Tyr
        145                      150                      155

agt tca gct gca tcc tac aca gat agc tct gat gat gag gtt tct ccc    527
Ser Ser Ala Ala Ser Tyr Thr Asp Ser Ser Asp Asp Glu Val Ser Pro
160                      165                      170                      175

cga gag aag cag caa acc aac tcc aag ggc agc agc aat ttc tgt gtg    575
Arg Glu Lys Gln Gln Thr Asn Ser Lys Gly Ser Ser Asn Phe Cys Val
                180                      185                      190

aag aac atc aag cag gca gaa ttt gga cgc cgg gag att gag att gca    623
Lys Asn Ile Lys Gln Ala Glu Phe Gly Arg Arg Glu Ile Glu Ile Ala
                195                      200                      205

gag caa gac atg tct gct ctg att tca ctc agg aaa cgt gct cag ggg    671
Glu Gln Asp Met Ser Ala Leu Ile Ser Leu Arg Lys Arg Ala Gln Gly
        210                      215                      220

gag aag ccc ttg gct ggt gct aaa ata gtg ggc tgt aca cac atc aca    719
Glu Lys Pro Leu Ala Gly Ala Lys Ile Val Gly Cys Thr His Ile Thr
        225                      230                      235

gcc cag aca gcg gtg ttg att gag aca ctc tgt gcc ctg ggg gct cag    767
Ala Gln Thr Ala Val Leu Ile Glu Thr Leu Cys Ala Leu Gly Ala Gln
240                      245                      250                      255

tgc cgc tgg tct gct tgt aac atc tac tca act cag aat gaa gta gct    815
Cys Arg Trp Ser Ala Cys Asn Ile Tyr Ser Thr Gln Asn Glu Val Ala
                260                      265                      270

gca gca ctg gct gag gct gga gtt gca gtg ttc gct tgg aag ggc gag    863
Ala Ala Leu Ala Glu Ala Gly Val Ala Val Phe Ala Trp Lys Gly Glu
                275                      280                      285

tca gaa gat gac ttc tgg tgg tgt att gac cgc tgt gtg aac atg gat    911
Ser Glu Asp Asp Phe Trp Trp Cys Ile Asp Arg Cys Val Asn Met Asp
        290                      295                      300

ggg tgg cag gcc aac atg atc ctg gat gat ggg gga gac tta acc cac    959
Gly Trp Gln Ala Asn Met Ile Leu Asp Asp Gly Gly Asp Leu Thr His
        305                      310                      315

tgg gtt tat aag aag tat cca aac gtg ttt aag aag atc cga ggc att   1007
Trp Val Tyr Lys Lys Tyr Pro Asn Val Phe Lys Lys Ile Arg Gly Ile
320                      325                      330                      335

gtg gaa gag agc gtg act ggt gtt cac agg ctg tat cag ctc tcc aaa   1055
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gct ggg aag ctc tgt gtt ccg gcc atg aac gtc aat gat tct gtt acc    1103
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aaa cag aag ttt gat aac ttg tac tgc tgc cga gaa tcc att ttg gat    1151
Lys Gln Lys Phe Asp Asn Leu Tyr Cys Cys Arg Glu Ser Ile Leu Asp
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ggc ctg aag agg acc aca gat gtg atg ttt ggt ggg aaa caa gtg gtg    1199
Gly Leu Lys Arg Thr Thr Asp Val Met Phe Gly Gly Lys Gln Val Val
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gtg tgt ggc tat ggt gag gta ggc aag ggc tgc tgt gct gct ctc aaa    1247
Val Cys Gly Tyr Gly Glu Val Gly Lys Gly Cys Cys Ala Ala Leu Lys
400             405             410             415

gct ctt gga gca att gtc tac att acc gaa atc gac ccc atc tgt gct    1295
Ala Leu Gly Ala Ile Val Tyr Ile Thr Glu Ile Asp Pro Ile Cys Ala
            420             425             430

ctg cag gcc tgc atg gat ggg ttc agg gtg gta aag cta aat gaa gtc    1343
Leu Gln Ala Cys Met Asp Gly Phe Arg Val Val Lys Leu Asn Glu Val
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atc cgg caa gtc gat gtc gta ata act tgc aca gga aat aag aat gta    1391
Ile Arg Gln Val Asp Val Val Ile Thr Cys Thr Gly Asn Lys Asn Val
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gtg aca cgg gag cac ttg gat cgc atg aaa aac agt tgt atc gta tgc    1439
Val Thr Arg Glu His Leu Asp Arg Met Lys Asn Ser Cys Ile Val Cys
            465             470             475

aat atg ggc cac tcc aac aca gaa atc gat gtg acc agc ctc cgc act    1487
Asn Met Gly His Ser Asn Thr Glu Ile Asp Val Thr Ser Leu Arg Thr
480             485             490             495

ccg gag ctg acg tgg gag cga gta cgt tct cag gtg gac cat gtc atc    1535
Pro Glu Leu Thr Trp Glu Arg Val Arg Ser Gln Val Asp His Val Ile
            500             505             510

tgg cca gat ggc aaa cga gtt gtc ctc ctg gca gag ggt cgt cta ctc    1583
Trp Pro Asp Gly Lys Arg Val Val Leu Leu Ala Glu Gly Arg Leu Leu
            515             520             525

aat ttg agc tgc tcc aca gtt ccc acc ttt gtt ctg tcc atc aca gcc    1631
Asn Leu Ser Cys Ser Thr Val Pro Thr Phe Val Leu Ser Ile Thr Ala
            530             535             540

aca aca cag gct ttg gca ctg ata gaa ctc tat aat gca ccc gag ggg    1679
Thr Thr Gln Ala Leu Ala Leu Ile Glu Leu Tyr Asn Ala Pro Glu Gly
            545             550             555

cga tac aag cag gat gtg tac ttg ctt cct aag aaa atg gat gaa tac    1727
Arg Tyr Lys Gln Asp Val Tyr Leu Leu Pro Lys Lys Met Asp Glu Tyr
560             565             570             575

gtt gcc agc ttg cat ctg cca tca ttt gat gcc cac ctt aca gag ctg    1775
Val Ala Ser Leu His Leu Pro Ser Phe Asp Ala His Leu Thr Glu Leu
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aca gat gac caa gca aaa tat ctg gga ctc aac aaa aat ggg cca ttc   1823
Thr Asp Asp Gln Ala Lys Tyr Leu Gly Leu Asn Lys Asn Gly Pro Phe
            595             600             605

aaa cct aat tat tac aga tac taa tggaccatac taccaaggac cagtccacct   1877
Lys Pro Asn Tyr Tyr Arg Tyr
            610             615

gaaccacaca ctctaaagaa atattttta agataacttt tattttcttc ttactccttt   1937

cctcttgatt tttttcctat aatttcattc ttgttttttc atctcattat ccaagttctg   1997

cagaccacac aggaacttgc ttcatggctc tttagatgaa atagaagttc agggtccctc   2057

actctagtca ctaaagaagg attttactcc cccagcccag aaaggtgatt cttctcttta   2117

ccatttctgg ggactttagt cttaattagg taccttatta acaggaaatg ctaaggtacc   2177

ttctctgtgg aacaatctgc aatgtctaaa tcgccttaaa agagcccatt tcttagctgc   2237

tgaaatcagt gctctttcac ttcttcagag aagcagggat ggtacctacc cggcaggtag   2297

gttagatgtg ggtggtgcat gttaatttcc cttagaagtt ccaagccctg tttcctgcgt   2357

aaaggtggta tgtccagttc agagatgtgt ataatgagca tggcttgtta agatcaggag   2417

gcccacttgg atttatagta tagcccttcc tccactccca ccagacttgc tcatttttcg   2477

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Ala Thr Ala Pro Gln Lys Pro Thr Gln Leu Asp Ala Gly Ala Gly Arg
            35                  40                  45

Arg Val Gly Asp Arg Val Ser Glu Gly Ala Ala Arg Ala Gly Gly Arg
      50                  55                  60

Ala Pro Glu Gly Glu Arg Gly Gly Gly Gly Ser Ala Ala Gly Arg
  65                  70                  75                  80

Ala Gly Gly Gly Met Ser Met Pro Asp Ala Met Pro Leu Pro Gly Val
                  85                  90                  95

Gly Glu Glu Leu Lys Gln Ala Lys Glu Ile Glu Asp Ala Glu Lys Tyr
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Ser Phe Met Ala Thr Val Thr Lys Ala Pro Lys Lys Gln Ile Gln Phe
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Ser Ala Ala Ser Tyr Thr Asp Ser Ser Asp Asp Glu Val Ser Pro Arg
                165                 170                 175
Glu Lys Gln Gln Thr Asn Ser Lys Gly Ser Ser Asn Phe Cys Val Lys
                180                 185                 190
Asn Ile Lys Gln Ala Glu Phe Gly Arg Arg Glu Ile Glu Ile Ala Glu
                195                 200                 205
Gln Asp Met Ser Ala Leu Ile Ser Leu Arg Lys Arg Ala Gln Gly Glu
    210                 215                 220
Lys Pro Leu Ala Gly Ala Lys Ile Val Gly Cys Thr His Ile Thr Ala
225                 230                 235                 240
Gln Thr Ala Val Leu Ile Glu Thr Leu Cys Ala Leu Gly Ala Gln Cys
                245                 250                 255
Arg Trp Ser Ala Cys Asn Ile Tyr Ser Thr Gln Asn Glu Val Ala Ala
                260                 265                 270
Ala Leu Ala Glu Ala Gly Val Ala Val Phe Ala Trp Lys Gly Glu Ser
                275                 280                 285
Glu Asp Asp Phe Trp Trp Cys Ile Asp Arg Cys Val Asn Met Asp Gly
    290                 295                 300
Trp Gln Ala Asn Met Ile Leu Asp Asp Gly Gly Asp Leu Thr His Trp
305                 310                 315                 320
Val Tyr Lys Lys Tyr Pro Asn Val Phe Lys Lys Ile Arg Gly Ile Val
                325                 330                 335
Glu Glu Ser Val Thr Gly Val His Arg Leu Tyr Gln Leu Ser Lys Ala
                340                 345                 350
Gly Lys Leu Cys Val Pro Ala Met Asn Val Asn Asp Ser Val Thr Lys
                355                 360                 365
Gln Lys Phe Asp Asn Leu Tyr Cys Cys Arg Glu Ser Ile Leu Asp Gly
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Leu Lys Arg Thr Thr Asp Val Met Phe Gly Gly Lys Gln Val Val Val
385                 390                 395                 400
Cys Gly Tyr Gly Glu Val Gly Lys Gly Cys Cys Ala Ala Leu Lys Ala
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Leu Gly Ala Ile Val Tyr Ile Thr Glu Ile Asp Pro Ile Cys Ala Leu
                420                 425                 430
Gln Ala Cys Met Asp Gly Phe Arg Val Val Lys Leu Asn Glu Val Ile
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Arg Gln Val Asp Val Val Ile Thr Cys Thr Gly Asn Lys Asn Val Val
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Thr Arg Glu His Leu Asp Arg Met Lys Asn Ser Cys Ile Val Cys Asn
465             470             475             480

Met Gly His Ser Asn Thr Glu Ile Asp Val Thr Ser Leu Arg Thr Pro
            485             490             495

Glu Leu Thr Trp Glu Arg Val Arg Ser Gln Val Asp His Val Ile Trp
            500             505             510

Pro Asp Gly Lys Arg Val Val Leu Leu Ala Glu Gly Arg Leu Leu Asn
            515             520             525

Leu Ser Cys Ser Thr Val Pro Thr Phe Val Leu Ser Ile Thr Ala Thr
    530             535             540

Thr Gln Ala Leu Ala Leu Ile Glu Leu Tyr Asn Ala Pro Glu Gly Arg
545             550             555             560

Tyr Lys Gln Asp Val Tyr Leu Leu Pro Lys Lys Met Asp Glu Tyr Val
            565             570             575

Ala Ser Leu His Leu Pro Ser Phe Asp Ala His Leu Thr Glu Leu Thr
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Asp Asp Gln Ala Lys Tyr Leu Gly Leu Asn Lys Asn Gly Pro Phe Lys
            595             600             605

Pro Asn Tyr Tyr Arg Tyr
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